Abstract from the workshop

genetic conservation and management of sparsely distributed trees and bushes. Held 15-17 September 2008, Sorø, Denmark

Kafé, Isabelle Skarvig

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Abstracts from the workshop:

Genetic conservation and management of sparsely distributed trees and bushes

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Held 15-17 September 2008, Sorø, Denmark

Edited by Isabelle Skarvig Kafé

FACULTY OF LIFE SCIENCES
UNIVERSITY OF COPENHAGEN

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Abstracts from the workshop: Genetic conservation and management of sparsely distributed trees and bushes, 15-17 September 2008, Sorø, Denmark

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INTRODUCTION

Background
Wide scale planting based on seeds from non-local seed sources has been practised in Europe for years. Consequently, the gene pool of many woody species consists of 'islands' of indigenous populations separated by cultivated land with planted individuals of non-native genetic origin. The wide scale introduction of plants of non-local origin may cause serious conservation problems because the local gene pools can be swapped by the introduced plants. This may further lead to outbreeding depression and loss of genetic structures at the population level. Species with restricted gene pools are likely to be particularly sensitive as they may already be negatively influenced by historic founder effects and small population sizes.

Non-planted, sparsely distributed species will not be influenced by such influx of non-local gene pools, but may on the other hand suffer from genetic processes associated with small population sizes as a result of fragmentation of their habitats. For such species increase of their effective population sizes would be favourable.

Hybridisation with introduced species can be a problem for both planted and non-planted species.

The aim of the workshop was to discuss how gene conservation effort can benefit from landscape plantings that is based on seeds and seedlings representing the local genetic resources rather than non-local ones. Can landscape plantings support an evolutionary conservation programme, if based 'on genetically sound practices'?

The objectives of the meeting were to:

- Present and discuss knowledge regarding genetic structures, reproductive systems and genetic dynamics of sparsely distributed European woody plant species
- Present and discuss experience from ongoing programmes integrating conservation and genetic management of sparsely distributed European woody plant species
- Develop thoughts and ideas for further coordinated research efforts, which can support development of 'genetically sound practices' as well as integrated conservation and utilization programmes for scattered woody species in Europe.

Apart from the one-day field trip to the island of Møn, the workshop
Included the following sessions

- **Genetic patterns and processes**
- **The use of genetic markers in conservation**
- **Effects of climate changes**
- **Experiences from European programmes on integrated conservation and utilization of genetic resources**
- **Ideas for future cooperation**

The workshop was held 15. – 17. September 2008 at Kongskilde Friluftsgård, Sorø, Denmark.

We are happy to present the abstracts given by the researchers from eleven countries who participated the workshop.

The meeting was financed by GENECAR, which is one of four research networks established by the Nordic Forest Research Co-operation Committee and the Nordic forest research institutes to promote cooperation in forest research.

Erik Dahl Kjær, Professor
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Forest & Landscape Denmark. University of Copenhagen.

Ditte C. Olrik, Ph.D.
Danish Forest and Nature Agency

PROGRAMME

Monday, 15 September 2008

Morning	9:00 – 10:00 Registration 10:00 – 10:15 Welcome and introduction 10:15 – 12:30 Session 1 "Genetic patterns and processes" 10:15 – 11:00 Key note presentation by Dr. Rémy Petit 11:20 – 12:20 Presentations 1) Tor Myking "Genetic variation in northern marginal *Taxus baccata* populations" 2) Heike Liesebach "Chloroplast DNA diversity in red dogwood (*Cornus sanguinea* L.) in Europe" 3) Sanna Black-Samuelsson "Genetic diversity in *Ulmus glabra* – lessons from Sweden and Italy"
Afternoon	13:30 - 14:10 Presentations (continued) 4) Lene R. Nielsen "Pollen-mediated gene flow among individuals of wych elm (*Ulmus glabra*) in forest and open land after the influence of Dutch elm disease" 5) Ditte Olrik "Colonization of an open heath land by *Quercus robur*: where do the seeds come from?" 14:10 – 14:30 Introduction to Suserup Forest by Jens Emborg and Morten Christensen with focus on results from studies on species dynamics 14:30 – 17:30 Guided walk in Suserup Forest by Jens Emborg and Morten Christensen Suserup Forest is one of the last semi-natural forests of Denmark, and has been subject to very little direct human inference during the last century. The forest is located within walking distance from Kongskilde Friluftsgård.
Evening	19:30–20:30 Presentations (continued) 6) Pekka Vakkari "Gene flow within and among pedunculate oak stands in Finland" 7) Daniela Salvini "Seed dispersal distances: an example from the *Quercus petraea/pubescens* complex in Italy" 8) Erik D. Kjær "Genetic variation in resistance of natural Ash populations in Denmark against novel die-back"

Tuesday, 16 September 2007

Whole day excursion to the island, Møn, which is a unique geological element in the Danish landscape and hosts various spectacular habitats: Visit *in situ* and *ex situ* gene conservation populations and seed orchards.
Link: http://www.moensklint.dk/default.asp?MenuID=877&vis=Jydelejet

Wednesday, 17 Septbember 2007

Morning	8:30 – 10:30 Session 2 "The use of genetic markers in conservation" 9:30 – 10:10 Presentations 1) Jörg Kleinschmit "Gene flow in conservation seed orchards of *Malus sylvestris* and *Sorbus domestica*" 2) Joukje Buiteveld "Application of molecular markers in the Dutch conservation program: a case study in *Ulmus*" 10:30 – 11:30 Session 3: "Effects of climate changes" 1) Øystein Johnsen "Epigenetic memory in trees - present research and plans for future" 2) Raquel Diaz "Genetic Variation in Adaptive Traits of *Prunus avium* clones from Northern Spain" 3) Jon K. Hansen "Climate change: study norm of reactions for European sessile oak populations based on results from an European series of field trials"
Afternoon	12:30 – 13:30 Session 4 "Experiences from European programmes on integrated conservation and utilization of genetic resources" 1) Kristine Vander Mijnsbrugge "Conservation programme of autochthonous woody plants in Flanders" 2) Lars N. Hansen / Erik D. Kjær "Genetic conservation and management of Danish Woody Species" 3) Other countries… 13:45 – 15:30 Ideas for future cooperation's 1) Introduction by Bjerne Ditlevsen 2) Discussion of ideas for future cooperation

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ABSTRACTS
(in order of presentation)

Tree evolution and conservation

Rémy J. Petit
INRA, UMR1202 Biodiversity Genes & Communities

Abstract
There are many good reasons to study how trees evolve compared to other organisms.
First, it is impossible to exaggerate the importance of trees in terrestrial ecosystems on our planet. They represent the bulk of the biomass and 20-25% of the total diversity of plants (there is an estimate of 60 to 80,000 species of trees, mostly in the tropics).

Second, better understanding their evolution should inform conservation strategies. Trees represent ancient lineages from which herbs have evolved repeatedly. But trees have also evolved repeatedly from herbaceous ancestors, for instance on oceanic islands. Since the tree habit has evolved many times, it is possible to investigate its evolutionary consequences. In particular, trees are long-lived organisms, so the question arises whether the lengthen generation times have evolutionary consequences, e.g. on the rate of evolution.

In 1916, Sinnott showed that there is a generation-time effect on evolution, with longer generations resulting in reduced rates of diversification. More recent studies based on DNA sequences have confirmed this early insight by showing that rates of molecular evolution are reduced in trees (Petit & Hampe 2006). If so, one would expect that trees have also reduced genetic diversity, as they should accumulate fewer mutations per unit of time. This prediction is at odds with the classical population genetics literature, based on allozymes, which has repeatedly reported large levels of genetic diversity in trees. There is therefore a need to account for this apparent paradox.

First, at the nucleotide level, trees have at most intermediate levels of variation compared to short-lived plants, so allozymes results might be in part misleading.

Second, trees have large population sizes (given their high rates of gene flow), so whatever diversity appears through mutation can persist and accumulate during extended periods of time (Hampe & Petit 2005).

Third, trees easily engage in interspecific crosses, which could drag substantial variation from related species.

Fourth, trees, being long-lived, do not withstand the deleterious effect of inbreeding: as a consequence, they have evolved a highly outcrossed mating system.

Finally, trees have prodigious reproductive capacities, so strong selection is possible during early life stages, potentially removing most inbred seedlings. Together, these characteristics make trees very resilient to many changes. In extreme examples, tree's genetic structure and diversity have remained nearly untouched since the Tertiary in areas where ice has not wiped out completely all forests (Magri et al. 2007, Petit et al. 2005, 2008).

Trees are also known to be very resilient to bottlenecks; for instance, invasive trees have typically preserved a significant part of the genetic diversity found in the native range, a likely consequence of their extended pollen gene flow. However, genetically depauperate trees exist. In Europe, *Pinus pinea*, the umbrella pine, is remarkable for its near complete lack of diversity at the nucleotide level (Vendramin et al. 2008). The existence of variation for adaptive traits in this species suggests that epigenetic modifications might be involved.

In conclusion, I suggest that a good understanding of the specificities of trees in terms of evolution should be taken into account in management. Such management should aim at understanding the underlying biological processes rather than focusing on descriptive diversity statistics for prioritizing and managing conservation areas. In addition to providing this general context, genetics also provides markers that can be used with great effects in conservation and management programs, to track plants or wood for conservation and management purposes (identification of introduced material, of species, of geographic origin, of clones or hybrids, of transgenes).

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Genetic variation in northern marginal *Taxus baccata* populations. Implications for conservation

Tor Myking[1], Pekka Vakkari[2] and Tore Skrøppa[1]

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Abstract
Taxus baccata is a dioecious, evergreen gymnosperm with a wide but scattered distribution in Europe. Pollen is dispersed by wind, and seed dispersal is mediated by birds.

We studied genetic structure in 13 *T. baccata* populations of the northern range margin in coastal areas of Norway by means of 15 isoenzyme loci.

The average observed and expected heterozygosities were 0.143 and 0.149, respectively. The genetic differentiation was considerable (Fst = 0.146), especially taken into account the limited study area.

The average fixation index was 0.039, but with consistently higher values (0.122 - 0.23) in the northernmost populations, suggesting inbreeding.

It is argued that if the present extensive browsing by game reduces future population sizes of *T. baccata*, the presently modest gene flow (Nm = 1.46) may be reduced to a level in which fixation becomes more prevalent and genetic variation gets lost. Although *T. baccata* is generally considered a declining species, there is no imminent risk of extinction in the northern distribution area.

Chloroplast DNA diversity in red dogwood (*Cornus sanguinea* L.) In Europe

Heike Liesebach & Bernhard Götz
vTI - Institute of Forest Genetics

Abstract
The red dogwood *Cornus sanguinea L*. is a deciduous shrub of the temperate and Mediterranean zones. It is often used in landscape gardening for miscellaneous purposes.

Chloroplast DNA markers (cpDNA haplotypes) are a very potential marker type to characterise the large scale variation pattern within the natural range of a species.

In this study, a total of 86 populations and 673 individuals were sampled all over Europe. Eight different haplotypes were recognised by combinations of several PCR-RFLP patterns. They are divided into 3 groups of related types. There is no association between these 3 groups and their geographic occurrence within the tested material.

One haplotype strongly dominates in the whole distribution area. It takes nearly 90 percent whereas the remaining seven haplotypes together reach to approximately 10 percent. Besides the low number of haplotypes, the total genetic variation HT = 0.15 is much lower in *Cornus sanguinea* compared to other European tree and shrub species. Despite the low level of variation, several cases of introduced populations could be detected. Other haplotypes than the common type are found only in narrow areas. This result indicates that after the colonisation of the European continent only a very restricted gene flow could have taken place.

Genetic diversity in elms - lessons and visions from Sweden and Italy

Sanna Black-Samuelsson & Luisa Ghelardini. Department of plant biology and forest genetics, SLU, Uppsala, Sweden. 2008.

Abstract
Even after decades of persistent research and breeding for resistant clones, Dutch elm disease (DED) continues its explosive spread. Complex interactions between the fungi (*Ophiostoma*), the vector (*Scotylus* beetle) and the environment determine if the elm gets infected. A phenological trait - timing of budburst - seems to be one important factor involved in the susceptibility to DED: Southern elm clones with the quickest budburst in field trials were the least susceptible to the disease. Phenological data also play an important role for observing biological effects of climate change and how elms react on these changes.

Therefore, we are now investigating induction of dormancy in *U. glabra* in a growth chamber based experiment. We also have some visions for future elm research and co-operation: I) to further investigate how budburst time is related to the tree's susceptibility to DED; and II) to construct a genetic linkage map in elms in order to identify the putative genes linked to resistance to DED.

Pollen-mediated gene flow among individuals of wych-elm (*Ulmus glabra*) in forest and open land after the influence of Dutch elm disease

Lene Rostgaard Nielsen and Erik Dahl Kjær
Forest & Landscape Denmark. University of Copenhagen.

Abstract
Dutch elm disease is a well known example of an infectious disease that has quickly eliminated large numbers of individuals of several wild species (the elms) leaving the remaining populations highly fragmented. The present study seeks to reveal effects of density decrease on mating system and gene flow in *Ulmus glabra*.

With four polymorphic microsatellite markers we used the programme MLTR to estimate the outcrossing rate in a sample of trees from a dense forest (Suserup Forest) and from seven solitary trees found scattered around in Denmark. In both cases (forest and open land) we found no indications of natural selfing (outcrossing rates = 1.0). With the programme GERUD we estimated the minimum number of fathers per offspring array in forest trees and solitary trees. This showed that mother trees received pollen from at least three different fathers no matter location. Gene flow parameters were estimated for the forest population with the programme package POLDISP. This revealed that the average pollen dispersal distance under forest conditions was around 100 metres. The solitary trees in the open land had distances to the nearest potential pollen donor in a range from 100m to more than 500m. This suggests that pollen in the open land on average travel further than in a dense forest. In Suserup Forest the canopy layer is dominated by other tree species (*Fagus*, *Quercus* and *Fraxinus*), which to some extent may inhibit long distance pollination. We further found that very young trees produced fruits. Reproduction at a young age may be a key stone in the survival of *U. glabra* due to the infection biology of Dutch elm disease.

Colonization of an open heath land by *Quercus robur:* Where do the seeds come from?

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Abstract
In order to quantify seed flow distances from a population of *Quercus robur*, we identified a population of 147 trees growing next to an open heath land hosting many young oak seedlings. We sampled 107 seedlings from the open area in four transects (6 m-700 m from the source population), and revealed likely parentage of seedlings by microsatellite genotyping data. We found seedlings from the source population at distances up to 700 meters, which was the furthest distance from the source population at which seedlings were sampled. However, we also found that approximately half of the seedlings did not originate from the source population, but must have been recruited from more distant oak populations, growing at least 500 meters away in a direction opposite to the transects from the source population. We conclude, that it will be difficult to control and influence the genetic origin and composition of natural regeneration of *Quercus robur* through selection and management of seed trees in vicinity of areas to be afforested by natural recruitment, as seeds for colonisation of open areas apparently are recruited from trees at the landscape level, rather than from a fine scale border level. The study suggests that genetic bottlenecks and/or founder effects in *Quercus robur* regeneration in the fragmented Danish forest landscape are likely to be counteracted by substantial seed dispersal over time across landscapes. The results fit well with reports of birds often transporting acorns several hundred meters away from seed parents.

Gene flow within and among pedunculate oak (*Quercus robur*) stands in Finland

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Abstract
Four pedunculate oak stands and three small tree groups (3, 4, and 10 trees) in southern Finland were studied for the pollination pattern within stands and for the amount of immigrating pollen. The larger stands included 2 unmanaged natural and 2 managed stands, where Norway spruces were cut, resulting in a sparse oak stand.

All trees of reproducing age were genotyped and acorns collected from 6 - 22 trees from the stands. In the small groups acorns were collected from 2, 3 and 8 trees. Seedlings were genotyped and candidate fathers or foreign pollen were identified using 12 microsatellite loci.

Pollination within the stands was observed to be far from panmixia, progenies of single trees were usually dominated by one or two neighbouring trees. Distribution of the fathers was more even in the managed stands. Amount of immigrating pollen was very low in most cases (2-10%), only within the main distribution area in Turku the gene flow was higher, 60-70% of immigrating pollen. The low level of gene flow may give rise to inbreeding within the stands.

Seed dispersal distances: an example from the *Quercus petraea/ Q. pubescens* complex in Italy

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Abstract
Effective oak acorn dispersal was analysed within a Mediterranean mixed broadleaved forest in central Italy, by means of parentage analysis. Our study species, *Q. petraea* and *Q. pubescens*, are closely related and largely interfertile. In order to study their seed dispersal pattern, we chose a study area within a natural forest, in which we had sampled all trees belonging to the *Q. petraea/Q. pubescens* complex and collected genetic material from a range of seedlings. Trees and natural regeneration (295 and 389 individuals respectively) were positioned and genotyped using five microsatellite markers. Genotypically compatible candidate parents for the natural regeneration were detected according to a total exclusion criterion. For each seedling having at least one candidate parent within the sampled area we chose the closest candidate and measured its distance from the seedling (MD), which provides a conservative estimate of the effective seed dispersal distance. In order to study the possible dispersal patterns that may have led to our results, we performed simulations based on different dispersal distances. Simulations consisted of the generation of a series of random haploid genotypes (gametes) sampled both from inside the sampled area (SA, from adult sampled trees) and from outside (allele frequencies of the population), followed by random mating. Seed dispersal was simulated both from SA and from outside, by assigning to genotypes randomly sampled distances from a positive Gaussian probability distribution and angles from a uniform probability distribution. Seeds that, after dispersal, resulted inside SA were analysed for parentage using the exclusion criterion and distances to closest genetically compatible candidates were calculated and grouped according to distance classes, in the same way as our empirical data. Assayed average dispersal distances ranged from 6.5 to 650 m. Simulated and empirical cumulative distributions of MD frequencies were compared by a Kolmogorov-Smirnov two sample statistical test. The empirical distribution did not differ significantly from the simulated ones for average distances ranging from 30 to 65 m, with closest fit for 40 m. Above and below such values differences were highly significant. The estimated acorn dispersal is in accordance with values obtained by previous studies on oaks based on parentage analysis and suggests the presence of secondary seed dispersal mediated by animals (possibly birds and rodents).

Keywords: effective seed dispersal, microsatellites, parentage analysis, *Q. petraea*, *Q. pubescens*

Significant genetic variation in *Fraxinus excelsior* for symptoms of novel ash dieback

Erik Dahl Kjær, Iben Thomsen, Lene Rostgaard Nielsen, Ditte C. Olrik and Ole Kim Hansen
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Abstract
A new, alarming tree health problem has appeared on ash (*Fraxinus excelsior* L.) in Poland and the Baltic countries for a decade causing devastating damages. Recently, the disease has caused severe damage in Sweden and Denmark, and symptoms are being reported from Germany, Austria, Czech Republic and Slovenia. The disease etiology of the dieback is not yet understood, but evidence points towards a new emerging infectious disease caused by a fungus (*Chalara fraxinea* Kowalski) acting as a necrotrophic pathogen and spreading across the forests and landscapes.

We present results regarding the potential presence of genetic resistance in natural ash populations based on assessments of clonal and progeny trials in Denmark. We find high frequency of genotypes exhibiting sever symptoms, but also genotypes that exhibit no or very limited level of symptoms. Observation in 2007 of 40 cloned genotypes (50 ramets / clone randomised at two sites) e.g. showed highly significant variation with symptom free ramets per clone varying from 0% to 94%. In 2008 the health decreased further, but the pattern remained the same with highly significant differences between clones, and consistence between the two sites.

An observed bimodal distribution of the tested clones was surprising. This could indicate action of few genes, because the clones originate from a few putative native Danish populations with no signs of strong population differentiation, and because a given population can include clones with both high and low susceptibility. However, resistance based on few major genes is unexpected for a necrotrophic pathogen.

The results from the progeny trials showed highly significant differences between half sib progenies suggesting that the genetic variation include a substantial additive component. Also here, we found no indication of genotype x environment interaction. Both results have important implication for the potential role of natural selection.

The implications of the results for future research efforts are discussed. Inoculation experiments to test whether symptom free genotypes exhibit resistance to infection by *Chalara fraxinea* remain to be done.

Gene flow in conservation seed orchards of *Sorbus domestica* L. and *Malus sylvestris* (L.) Mill.

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Abstract
Gene flow within and from outside conservation seed orchards (cso) is estimated by means of DNA microsatellite markers for the two species of the Rosaceae family.

For *Sorbus domestica* L. a cso with 49 clones, represented by 1-6 ramets each, and an adjacent alley with 83 individual were genotyped with four microsatellite loci. Additionally 7 half sib families of 4 different seed mother tree genotypes were analyzed. Minimum estimates of hybridization with genotypes form outside the cso are calculated. The median of minimum pollen transport distances for each seed mother tree was calculated for 50 seeds each. The hypothesis of homogeneous pollen clouds was tested for 3 ramets of a clone.

For 13.2% of the analyzed seeds a single individual was identified as potential pollen donor. 17.3 % of the seeds' pollen donors were definitely situated within the cso and 3.5% had pollen donors outside the cso. The median of minimum effective pollination distance for each half sib family ranged between 8 to 36 m. Significant differentiation of individual effective pollen clouds was found.

25 genotypes of a *Malus sylvestris* (L.) Mill. conservation seed orchard are compared with 21 cultivars to support classification according to morphological traits. Minimum estimates of hybridization with cultivars are calculated.

Application of molecular markers in the Dutch Conservation program: a case study of *Ulmus minor*

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Abstract
The Centre for Genetic Resources, the Netherlands (CGN) conducts, on behalf of the Dutch Government, statutory research task associated with genetic diversity and identity of species that are important for agriculture and forestry.

Its activities in forest genetic resources management are aimed at *ex situ* conservation, support for *in situ* conservation and promotion of the use of material in sustainable forest management.

For the *ex situ* conservation of trees and shrubs CGN closely collaborates with the State Forest Service and the Ministry of Agriculture, Nature and Food Quality. In spring 2006 a new gene bank for indigenous trees and shrubs has been opened in which material of more than 50 species has been included, representing over 400 *in situ* locations. In a number of these species molecular marker studies are applied to support the management of these genetic resources.

In *Ulmus minor* a microsatellite marker study was applied on 6 populations with the aim the characterize the genetic diversity of this species in the Netherlands and to support/refine the sampling strategy for setting up an *ex situ* collection that represents the gene pool of the *in situ* populations of *U. minor* well. The studied populations showed a modern genetic differentiation. Also a substantial number of clones occurred in the sampled material. The results support the influence of historical human plantings. The natural status of this species in The Netherlands and implications for conservation strategies are discussed.

Epigenetic memory in spruce – present research and plans for the future

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Abstract
We have recently found that temperature during zygotic embryogenesis and seed maturation regulates an "epigenetic memory" in the progeny, involving differential expression of genes that may regulate bud phenology and cold acclimation in Norway spruce.

Conditions colder than normal advance the timing whilst temperatures above normal delay the onset of these phenological processes. The altered performance lasts for many years. The seedlings do in fact remember the temperatures and photoperiod prevailing during zygotic embryogenesis and seed maturation.

We have shown for the first time that regenerated plants, cloned through somatic embryogenesis *in vitro*, express a memory of the temperatures applied during embryo development whilst growing in a common greenhouse environment.

The warmer the *in vitro* temperature applied, the later the regenerated plants formed terminal buds the second growth season after regeneration. The differences were very large, and similar in size to a provenance separation of 4 – 6 degrees of latitude.

Currently, we are looking for candidate genes which can regulate such a memory in Norway spruce, and some few interesting ones will be discussed.

The ultimate dream is to use such genes to identify parental members in breeding populations of Norway spruce that give rise to progenies with high (and low?) expression of the memory, fit to perform better (or more stable?) under future climatic conditions.

Genetic variation in adaptive traits of *Prunus avium* clones from Northern Spain

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Abstract
Tree species with large geographic distributions often show considerable variation in several adaptive traits, phenological and pathological ones among them. Wild cherry (*Prunus avium* L.) is one of the most valued forest tree species in Spain. However, little information is available about the intraspecific variation in different adaptive traits, and about their role in the adaptation to environmental factors in Spain. In the present work I studied the variation in two phenological (bud burst and flowering time) and one pathological (leaf spot susceptibility, caused by the fungus *Blumeriella jaapii* (Rehm) Arx.) trait of 155 clones selected within seven provenance regions from North Spain. Data were assessed in two clonal seed orchards located in Galicia (Northwestern Spain) during three years. The experimental design in both sites was a randomized complete block design with single tree-plots, and, 126 clones, and 7 blocks in the seed orchard 1 (SO1), and 77 clones, and 10 blocks in the seed orchard 2 (SO2). Forty-eight clones were in common in both seed orchards.

Significant differences were found among provenance regions and among clones within provenance regions for the studied traits. Two groups of provenance regions can be differentiated, one formed by clones from two inland provenance regions and another formed by the other clones. Bud burst, flowering time and leaf spot susceptibility, were highly correlated, so the earlier the clones flushed and flowered, the greater the susceptibility to cherry leaf spot. Correlation analyses between clonal mean values and geoclimatic data show a clinal variation for the studied traits. Altitude, annual mean temperature and total summer precipitation at the place of origin were the most important geoclimatic factors explaining bud burst, flowering time and cherry leaf spot susceptibility. Clones coming from lower altitudes, from places with higher annual mean temperatures and / or from sites with higher total summer precipitations, sprout their buds and flowers earlier and were more susceptible to cherry leaf spot.

These are important results for the conservation of wild cherry in Spain. Several individuals from two provenance regions out of the seven provenance regions studied, one from a high altitudinal area and the other from a low altitudinal place, should be included in the conservation program of *P. avium* in Spain, attending to the adaptive traits studied. Further studies should be done to evaluate these and other important traits, including also genotypes from other Spanish provenance regions.

Climate change: study norm of reactions for European sessile oak populations based on results from a European series of field trials

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Abstract
Preliminary results are presented from an evaluation of survival two years- and height five years establishment in a series of 13 field trials in France, Germany, Denmark and Great Britain established in 1992 with in total 19 sessile oak (*Quercus petraea* (Matt.) Liebl.) provenances from Belgium, German, Denmark, France, Great Britain, Norway, Poland and Turkey. Survival was registered two, or three years after establishment and height 5 years after establishment.

Genotype-environment interactions were found for survival after 2 years. Correlations at provenance level across sites were associated with high standard errors due to the few provenances, but differences in days with a temperature above 5 C between test sites tended to reduce the correlation between the sites. Genotype-environment interactions were also found for height after five years. Nevertheless, correlations at provenance level across sites were generally high with a 50% median of 0.88 and a range between 0.44 and 1.00 and it was not possible to explain the correlations across sites by differences between sites in climate.

Generally, the provenances showed decreasing height growth with increasing precipitation deficit at the test sites compared with the site of origin of the provenances and decreasing survival with decreasing yearly temperature at the test sites compared with the sites of origin. All over the field trials, it was possible to find provenances with better growth and survival and it was not possible to find any different reactions of provenances to changes in climate between test sites.

The production of autochthonous planting stock in Flanders

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Abstract
Native woody plant species are routinely planted in (re)forestation and landscape programs. But, successful establishment and survival in the long run may depend on where the seeds used to grow the planting stock are collected. There is evidence to suggest a home-site advantage for autochthonous populations and that non-local genotypes may be maladapted to local environmental conditions.

Furthermore, intraspecific hybridisation of local and non-local genotypes may have a negative impact on the genetic structures of local populations via mechanisms such as outbreeding depression. Negative impacts of improper seed choice for nursery planting stock may only be seen after many years, especially for long-lived and slow growing plants.

As several European countries face similar problems, the objective here is to outline the conservation measures that are taken in Flanders. Central issue is the production of autochthonous planting stock that should become widely available. The steps to achieve this issue will be discussed.

The Danish programme for domestication of native woody species

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([2]) Danish Forest and Nature Agency, Øresund

Abstact

Trees and shrubs of native species are planted with public support in the Danish forests, shelterbelts in agricultural land, and small woodlots for wildlife and amenities. Since 2001, Danish Centre for Forest, Landscape and Planning (University of Copenhagen) and The Danish Forest and Nature Agency have worked on an integrated approach to support wise use and management of genetic resources of such native woody plants species being planted in Denmark. The programme includes an array of activities including:

- Web-based information to nurseries and end-users on current knowledge about seed sources
- Research activities aiming at knowledge that can improve wise use of genetic resources
- Characterisation and mobilisation of local gene pools and development of suitable seed sources for large scale use
- Conservation and development of gene pools based on an evolutionary conservation approach.

An important part of these activities is organised within the 'The Danish programme for domestication of native woody species'. The core objective of this programme is to increase the success of Danish tree and shrub plantings through development and deployment of healthy and genetically diverse planting material of native woody species, and at the same time support wise management and conservation of genetic resources of our native woody species. The latter is targeted by taking genetic diversity, adaptive potential, and spatial genetic patterns into account, and thereby also serves as support to the on-going *in situ* conservation activities.

The genetic back-bone in the programme is seedlings grown from seed collected on trees or shrubs at different localities (putative local origin), planted in specialised progeny test/seed sources (so-called Breeding Seed Orchards). In the presentation we will discuss:

- The adaptive management approach: knowledge are generated and applied during the lifespan of the programme
- The BSO concept and its application
- Targeted level of diversity in the BSOs
- Sampling of Populations in the mobilisation process
- Genecological zonation and the applied number of breeding zones in the Danish programme
- Selection: Forward, backward, within families, between families, intensity, direction, timing?
- Deployment
- Advanced generations

The programme include establishment and management of 63 BSO's covering 30 species. More details on the seed source management, *ex situ* and *in situ* activities will be provided during the field trip to Møn.

Genetic conservation and management of sparsely distributed trees and bushes - interface between conservation and utilization

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Some ideas for future collaboration

In order to develop a closer collaboration between European genetics programmes the following points should be taken into consideration:

How to organize?

1. Establish contacts to programmes, institutions and individuals that are willing to cooperate
2. Agree on the structure / type of collaboration and on working procedures. It is proposed to establish an informal network, where the participants may collaborate or develop partnerships as needed
3. Who should organize and take responsibility for the initiation of the collaboration?

What are the objectives?

1. Compilation of a list of species that are included in the individual programmes in order to facilitate collaboration between programmes
2. Exchange of technical information related to the individual species, as e.g. seed handling techniques, grafting techniques etc.
3. Exchange of information on conservation, genetics improvement and seed production strategies applied in the individual programmes
4. Exchange of genetic material for research purposes or for conservation / breeding purposes

How to coordinate with – and avoid too much overlap - other initiatives?

1. EUFORGEN.
2. IUFRO
3. Others

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